Figure 1

Structure	of	v_H	domain	of	human	A6	antibody.

1 GAG. E	2 GTC V	3 CAG Q	4 CTG L	5 CAG Q	6 GAG E	7 TCT S	8 GGG G	9. GGA G	GGC	11 TTA L	12 GTC V	13 CAG Q	14 CCT P
15 GGG G		17 TCC S	18 CTG L	19 AGA R	CTC		22 TGT C			25 TCT S	26 GGA G	27 TTC F	28 ACC T
29 TTC F	30 AGT S	AGC	TAT Y	GCT	34 ATG M	CAC	TGG		38 CGC R	39 CAG Q		41 CCA P	42 GGG G
43 .					48 [:] GTT							54 S GGG	
K		L .	E		V		<u>A</u>	I	_S	S DR2	N	G	<u>G</u> .
К 56	G 57 ACA	L 58 TAC	E 59 TAC	Y 60 GCA		s 62 TCC	<u>A</u> 63 GTG	I 64 AAG	. C	S DR2	67 TTC	G 68	<u>G</u> .
56 AGC <u>S</u>	G 57 ACA T 71 AGA	58 TAC Y	59 TAC Y	9 60 GCA A	V 61 GAC D 75 AAG	\$ 62 TCC \$	63 GTG V	64 AAG K 78 CTG	65 GGC G	DR2 66 AGA R	81	68 ACC T	G 69 ATC I

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Figure 1 (continued)

100 a b c d e f g h 95 96 97 98 99 GAC AGG TTA AAA GTG GAG TAC TAT GAT AGT AGT TAT TAC E Y Y D S S G Y Y V K CDR3 m n o 101 102 103 104 105 105 107 1 k GTT TCT CGG TTC GGT GCT TTT GAT ATC TGG GGC CAA GGG ACA V S R F G A F D I W G Q G

108 109 110 111 112 113 ACG GTC ACC GTC TCA TCA T V T V S S

Figure 2

Structure of modified VH domain of human A6 antibody showing substitutions at position 44, 45, 47, 93 and 94. The NheI site is underlined.

1 GAG E	2 GTC V	CAG	CTG	CAG	GAG	TCT	GGG	GGA	10 GGC G	11 TTA L	12 GTC V	13 CAG Q	14 CCT P
15 GGG G	16 GGG G	17 TCC S	CTG	AGA	CTC	TCC	TGT	TCA	24 GCT A	AGC		27 TTC F	28 ACC T
29 TTC F	30 AGT S	AGC	TAT Y	GCT	ATG	CAC	TGG	GTC	38 CGC R	CAG	GCT	41 CCA P	
43 AAG K	GAA	45 CGT R	46 GAA E	GGT	GTT	TCA	GCT	ATT	S	AGT	AAT	54 5 GGG G	GGT
AGC	57 ACA T	TAC	TAC	GCA	GAC	TCC	GTG	AAG	GGC	AGA	67 TTC F	ACC	69 ATC I
TCC	71 AGA R	GAC	AAT	TCC	AAG	AAC	ACT	CTG	79 TAT Y	CTT	CAA	82 ATG M	
b AGT S	CTG	AGA	GCT	85 GAG E	GAC	ACG	88 GCT A	GTG	90 TAT Y	91 TAC Y	TGT		94 GCA A

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Figure 2 (continued)

95 96 97 98 99 100 a b c d e f g h
GAC AGG TTA AAA GTG GAG TAC TAT GAT AGT AGT GGT TAT TAC
D R L K V E Y Y D S S G Y Y

CDR3

i j k l m n o 101 102 103 104 105 105 107
GTT TCT CGG TTC GGT GCT TTT GAT ATC TGG GGC CAA GGG ACA
V S R F G A F D I W G Q G T

108 109 110 111 112 113 ACG GTC ACC GTC TCA TCA T V T V S S

Figure 3

Structure of VH domain of human A6 antibody. The mutated nucleotides spanning residues 7-48 to remove the recombination site are in bold and underlined.

1 GAG	2 GTC	3 CAA_	4 TTA	5 CAG	6 GAA	7 AGT	8. GGT	-9 GGC	10 GGA	11 CTG			14 CCA
	V	Q	L	Q	E	S	G	G	G	L	V	Q	P
15 CCA	16 GGA	17. TCC	18 CTG	19 AGA	20 CTC	21 TCC	22 TGT	23 TCA	24 GCC	25 TCT	26 · GGA	27 TTC	28 ACC
G		S	L	R	L	S.	C	S	A	S	G	F	Т
	· .			· .			2.5		2.0		4.0	41	42
29 TTC	30 AGT	AGC	32 TAT	GCT	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGG
	S	<u>s</u>	<u>Y</u>	A	M	H	W	V	R	Q	A	Ρ.	G .
			(DR1				•					
43	44	45	46	47	48	49	50	51 ·	52			54 5	
AAG	GGA G	CTG	GAA	TAT	GTT	TCA	GCT a	ATT T	AGT	AGT S	AAT N	GGG	GGT
ĸ	G .	Li	Ę.	1 .	V	5	Δ		C	DR2			 .
	•	•				60	60	<i>C</i> 4	6		67	60	69
56						6	h 1						0,0
AGC	57 aca	5.8 TAC	59 TAC	GCA	GAC	TCC	GTG	AAG	GGC	AGA	TTC	ACC	ATC
AGC	ACA	TAC	TAC	GCA	GAC	TCC	GTG	AAG	GGC	AGA	TTC	ACC	ATC I
AGC	57 ACA T	TAC	TAC	GCA	GAC	TCC	GTG	AAG	GGC	AGA	TTC	ACC	ATC
AGC S	ACA T	TAC Y	TAC Y 73	GCA A	GAC D	TCC S 76	GTG V 77	AAG K 78	GGC <u>G</u> 79	AGA R 80	TTC F	ACC T 82	ATC I a
AGC S 70 TCC	ACA T 71 AGA	TAC Y 72 GAC	TAC Y 73 AAT	GCA A 74 TCC	GAC D	TCC S 76 AAC	GTG V 77 ACT	AAG K 78 CTG	GGC G 79 TAT	AGA R 80 CTT	TTC F ·81 CAA	ACC T 82 ATG	ATC I a AGC
AGC S 70 TCC	ACA T	TAC Y 72 GAC	TAC Y 73 AAT	GCA A 74 TCC	GAC D	TCC S 76 AAC	GTG V 77 ACT	AAG K 78 CTG	GGC G 79 TAT	AGA R 80 CTT	TTC F ·81 CAA	ACC T 82 ATG	ATC I a AGC
AGC S 70 TCC S	ACA T 71 AGA R	TAC Y 72 GAC D	TAC Y 73 AAT N	GCA A 74 TCC S	GAC D	TCC S 76 AAC N	GTG V 77 ACT T	AAG K 78 CTG L	GGC G 79 TAT Y	AGA R 80 CTT L	TTC F 81 CAA Q	ACC T 82 ATG M	ATC I a AGC S
AGC S 70 TCC S	ACA T 71 AGA R	TAC Y 72 GAC D	TAC Y 73 AAT N	GCA A 74 TCC S	GAC D 75 AAG K	TCC S 76 AAC N	GTG V 77 ACT T	AAG K 78 CTG L	GGC G 79 TAT Y	AGA R 80 CTT L	TTC F 81 CAA Q	ACC T 82 ATG M	ATC I a AGC S

Figure 3 (continued)

GAC	AGG	TTA	98 AAA K	GTG	GAG	TAC	TAT Y_	GAT	AGT	AGT _.	GGT	TAT	TAC
						C1)K3						
GTT	TCT	CGG	l TTC F	GGT	GCT	TTT	GAT	ATC	TGG	GGC	CAA	GGG	ACA

108 109 110 111 112 113 ACG GTC ACC GTC TCA TCA T V T V S S

Figure 4

Structure of modified VH domain of human A6 antibody showing substitutions at position 44, 45, 47, 93 and 94. The mutated nucleotides spanning residues 7-48 to remove the recombination site as well as the NheI site are in bold and underlined.

GAG	GTC	CAA	$\mathbf{A}\mathbf{T}\mathbf{T}$	CAG	GAA	AGT	GGT	9 GGC	GGA	CTG	12 GTG V	13 <u>CAA</u> O	14 <u>CCA</u> P
E	V	Q	L	Q	Е	S	(.	G	G	ப	V	Q	P
GGA	GGA	TCC	CTG	AGA	CTC	TCC	TGT.	TCA	GCT	AGC	26 GGA G	TTC.	28 ACC T
TTC	AGT	AGC S	TAT	GCT A	ATG M	CAC	TGG	GTC	CGC	CAG	40 GCT A	CCA	GGG
43	44	45	46	47	48	49	50	51	52	a !	53 :	54 5	55
43 AAG	44 GAA	CGT	GAA	GGT	GTT	TCA	GCT	ATT	AGT	AGT	53 S AAT	GGG	GGT
AAG	44 GAA E	CGT	GAA	GGT	GTT	TCA S	GCT A	ATT I	AGT S	AGT S	53 5 AAT N	GGG	GGT
AAG	GAA	CGT	GAA	GGT	GTT	TCA S	GCT A	ATT	AGT S	AGT S	TAA	GGG	GGT
AAG K	GAA E	CGT R	GAA E 59	GGT G	GTT V 61	TCA S	GCT A	ATT I 64	AGT S C	AGT S DR2	AAT N	GGG G	GGT G 69
AAG K 56	GAA E 57	CGT R 58	GAA E 59	GGT G 60 GCA	GTT V 61 GAC	TCA S 62 TCC	GCT A 63 GTG	ATT I 64 AAG	AGT S C 65 GGC	AGT S DR2 66 AGA	AAT N · 67 TTC	GGG G 68 ACC	GGT G 69 ATC
AAG K 56	GAA E 57	CGT R 58	GAA E 59	GGT G 60 GCA	GTT V 61 GAC	TCA S 62 TCC	GCT A 63 GTG	ATT I 64 AAG	AGT S C 65 GGC	AGT S DR2 66 AGA	AAT N	GGG G 68 ACC	GGT G 69 ATC
AAG K 56	GAA E 57	CGT R 58	GAA E 59	GGT G 60 GCA	GTT V 61 GAC	TCA S 62 TCC	GCT A 63 GTG	ATT I 64 AAG	AGT S C 65 GGC	AGT S DR2 66 AGA	AAT N · 67 TTC	GGG G 68 ACC	GGT G 69 ATC

Figure 4 (continued)

86 87 88 89 90 91 92 93 94 84 85 83 AGT CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT GCA GCA V Y C \mathbf{T} Α ·Y Α E D R 100 a b c d e £ 99. 97 98 96 GAC AGG TTA AAA GTG GAG TAC TAT GAT AGT AGT TAT TAC Y Y D S ν. \mathbf{E}_{-} CDR3 101 102 103 104 105 105 107 0 k 1 m n GTT TCT CGG TTC GGT GCT TTT GAT ATC TGG GGC CAA GGG ACA F G A F D I W G Q \mathbf{T} 108 109 110 111 112 113 ACG GTC ACC GTC TCA TCA T V T VS

Figure 5

kDa	1
209 124	
80	
49.1	e Bey (n. 1941) Le la companya (n. 1941)
34.8	াইকিল কৈ শৈলুৰ দেকন
28.9	
20.6	
7.1	and the same of th

2.

Figure 6

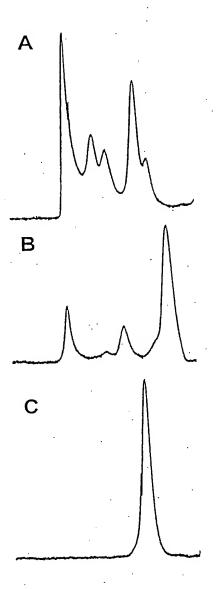
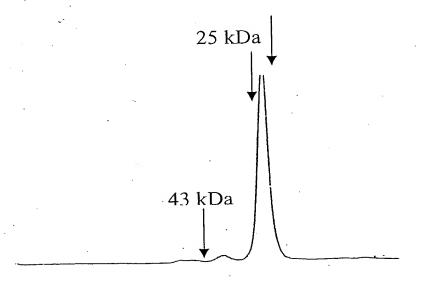
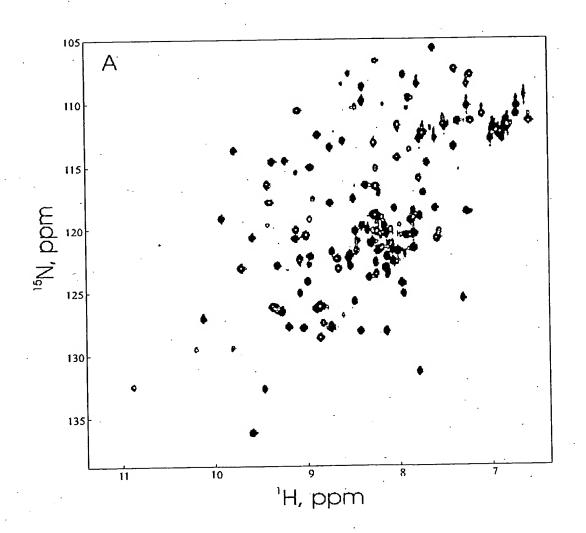


Figure 7



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Figure 8A



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Figure 8B

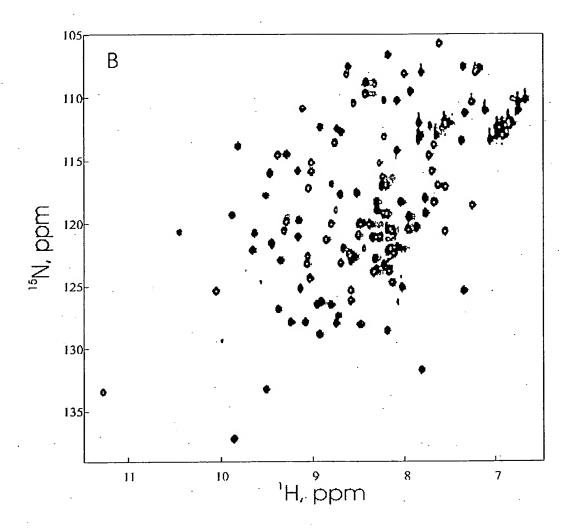


Figure 9

<u> A6VH</u>

				•			
Fr4	CDR3		Fr3	CDR2	Fr2	CDR1	Fr1
256	S100E	V93 K94		New Services	G44 L45 Y47	A 33	Property and
							<u> 46VH.</u>
200	S100E	A93 A94	in ang ny mand di		E44 R45 G47	A33	igo egolia ari bigib
	C100E					<u>1C</u> င်း	<u>A6VH.</u>
		A93 A94	pova v ervet potenšavit		E44 R45 G47	: (6282998

Figure 10

Structure of modified VH domain of human A6 antibody showing substitutions at position 33, 44, 45, 47, 93, 94 and 100e.

1 GAG E	2 GTC V	3 CAG Q	4 CTG L	CAG	6 GAG E	TCT	GGG	9 GGA G	10 GGC G	11 TTA L		13 CAG Q	14 CCT P
15 GGG G	16 GGG G	17 TCC S		AGA		TCC	TGT		24 GCC A		GGA		28 ACC T
29 TTC F	30 AGT S	31 AGC S	TAT	TGT	ATG	CAC	TGG	GTC	38 CGC R	39 CAG Q	GCT	41 CCA P	42 GGG G
				DR1									-
43 AAG K	GAA		GAA		GTT		GCT	ATT	52 AGT S	AGT	AAT	GGG G	GGT
AGC	ACA	TAC	TAC	GCA	GAC	TCC	GTG	AAG	65 GGC <u>G</u>	66 AGA R	67 TTC F	68 ACC T	
	0								•				
70 TCC S	AGA	72 GAC D	73 AAT N	TCC	75 AAG K	AAC	ACT	CTG	TAT	80 CTT L			
b AGT S					GAC	ACG	GCT		90 TAT Y			93 GCA A	94 GCA A

Figure 10 (continued)

GAC	AGG	TTA	AAA	GTG	100 GAG E	TAC	TAT	GAT	AGT	TGC	GGT	
							R3					
-	TCT		TTC	GGT	n GCT A	TTT	GAT	ATC	TGG	GGC	CAA	ACA
				112 TCA								

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Figure 11

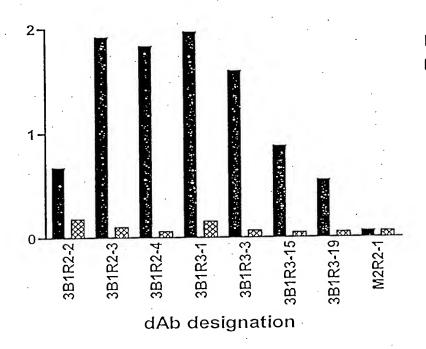
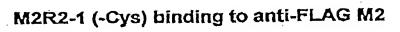


Figure 12



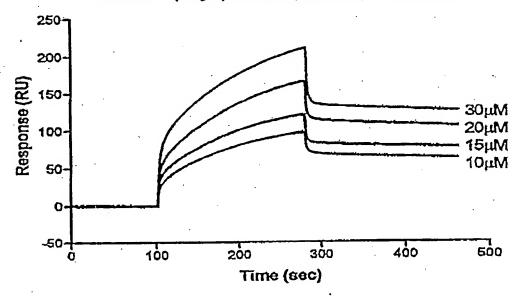


Figure 13

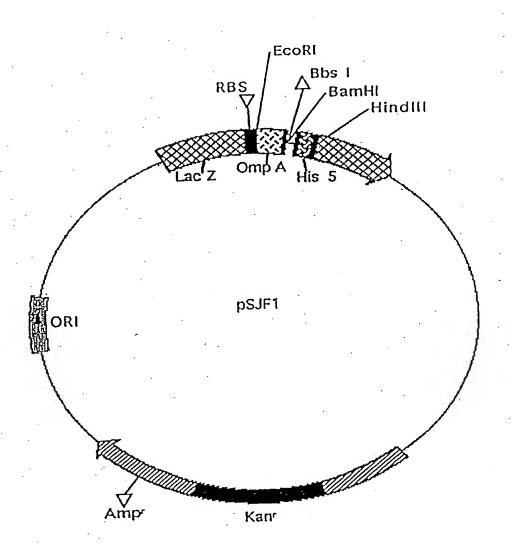


Figure 14

Structure of $V_{\rm H}$ domain of human A6 antibody. The mutated nucleotides spanning residues 7-48 to remove the recombination site are in bold and underlined.

	2 GTC				6 GAA				10 GGA	11 CTG	12 GT G	13 CAA	1·4 CCA
E	`V	Q	L	Q	E	S	G	G	G	L	V	Q	. P
15 GGA G		17 TCC S	18 CTG L		20 CTC L		TGT	23 TCA S	24 <u>GCT</u> A	25 AGC S	26 GGA G	27 TTC F	28 ACC T
29 TTC F	AGT	AGC	TAT	GCT	34 ATG M	CAC	TGG	GTC		39 CAG Q		41 CCA P	
				DR1	٠.								
43												54 5	
												GGG	
K	G	L .	Ε .	Υ .	V	S	<u>A</u>			DR2	N	G	<u>. G</u>
AGC	ACA	TAC	TAC	GCA	61 GAC D	TCC	GTG	AAG	GGC	AGA	TTC	68 ACC T	69 ATC I
												-	
		GAC	TAA	TCC	75 AAG K	AAC	ACT		TAT	CTT		ATG	a AGC S
		AGA			86 GAC D	ACG			TAT		92 TGT C	93 GTG V	94 AAA K

W G Q G T

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Figure 14 (contined)

95	96	97	98	99	100	a	b	С	d	е .	£	g	h
GAC	AGG	TTA	AAA	GTG	GAG	TAC	TAT	GAT	AGT	AGT	GGT	TAT	TAC
D	R	L	K	V	E	Y	Y	D	S	S	G	Y	<u>Y</u>
			•			CI	R3						
									103 TGG				

108 109 110 111 112 113 ACG GTC ACC GTC TCA TCA T V T V S S

V S R F G A F D I

Figure 15

